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Location/Qualifiers 1215 /organism="unknown" 15 a 8 c 25 g 26 t	Unknown. Unknown. Unknown. Unclassified. 1 (bases 1 to 215) 1 (bases 1 to 215) Bennett, A., Labavitch, J.M., Powell, A. and Stotz, H. Plant inhibitors of fungal polygalacturonases and their use to control fungal disease Patent: US 5569830-A 5 29-OCT-1996;	128278 215 bp DNA Sequence 5 from patent US 5569830. 128278 g1819054
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Eukaryotae; mitochondrial eukaryotes; Alveolata; hypotrichs; Stichotrichida; Oxytricha:

1 (bases 1 to 354)

Doak, T.G., Doerder, F.P., Jahn, C.L. and Herrick, G
A proposed superfamily of transposase genes: transposase genes:
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Bennett,A., Labavitch,J.M., Powell,A. and Stotz,H.
Plant inhibitors of fungal polygalacturonases and
control fungal disease
Patent: US 5569830-A 5 29-OCT-1996;
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hypotrichs;
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                                                                                                                                                                                                                                                                                                                     OFU89259 standard; DNA; INV; 354 BP. U89259; g18816/5 13-MAR-1997 (Rel. 51, Created) 13-MAR-1997 (Rél. 51, Last updated, Version Oxytricha fallax 57kD zinc finger/protein checds.
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/note="this is a bulk sequence that was gene
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/strain="9D1"
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                                           Doak T.G., Williams K., Seger J., Herrick G., protein-coding genes of the TBE1 family of ents in the ciliates Oxytricha fallax and O.
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a; Oxytrichidae; Oxytricha.
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Pred. No. 3.33e-03;
33; Mismatches 24
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nes 25; Conservative
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School of Med. Rm5C334, USA,
Location/Qualifiers
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1 (bases 1 to 354)
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Oxytricha fallax
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Doak, T.G., Williams, K.,
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/note="this is a bulk sequen
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/transposon="TBE1"
/note="this is a bulk sequence that was generated from
/note="this is a bulk sequence that was generated from
PCR product that represents many transposon templates"
                                             /organism="Oxytricha
/strain="9D1"
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/product="57kD zinc finger/protein
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/translation="HTRDLXKHLLKAHKKXXEXEXXXXXLKXLXKRKAREXXXXXXXX
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33; Mismatches 24
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USA, UT 84132, USA
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91881675
13-MAR-1997 (Rel. 51, Created)
13-MAR-1997 (Rel. 51, Last updated, Version 1)
Oxytricha fallax 57kD zinc finger/protein chimera
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"A proposed superfamily of transposase genes:
elements in ciliated protozoa and a common 'D35E' motif";
proc. Natl. Acad. Sci. U.S.A. 91:942-946(1994).
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hypotrichs; Stichotrichida; Oxytrichidae; Oxytricha
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/note="this is a bulk sequence that was generated from
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                           /product-"57kD zinc finger/protein chimera"
/transl_table-6
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 AXEXXXVXXXRNXLXSEXTKIMIKIQYKKIPVLAQIDLDTSLQSYLILEDSFDKKVIX
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/strain="9D1"
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ciliates Oxytricha fallax and O.
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Mismatches 36;
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                                 Carassius
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Cohen, I., Shani, Y. and Schwartz, M.
Cloning and characteristics of fish glial fibrillary acidic protein: implications for optic nerve regeneration
J. Comp. Neurol. 334 (3), 431-443 (1993)
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glial fibril.
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 Carassius
                                                                                       CRAGF1
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Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
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                                                                     1933
s auratus
                                                                                                                                                                                                                                                                                                                   /product="glial fibrillary acidic protein"
/db_xref="plD:g435739"
/translation="VDLDVSKPDLTTALKEIRAOFEAMATSNMOETEEWYRSKFADLT
DAASRNTEALROAKQEANEYRROIQGLTCDLESLRGSNESLERGLREMEERFTIETAG
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QNFTNLQFRDTSLDTKLTPEAHVKRSIVVRTVETRDGEIIKESTTERNDLP"
273 c 347 g 401 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Description: glial fibrillary acidic protein, GFAP, Method: conceptual translation with partial peptide sequencing. This sequence comes from Fig. 2"
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1..636
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adult retina
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(GFAP-1) mRNA,
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Pred. No. 3
38; Mismat
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Pred. No. 3.26e-01
0; Mismatches 1
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3.26e-01
CDNA to mRNA
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Best Local Similarity 77.8%;
                                                                                                                                                                          AUTHORS
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                                                                                                     Direct Submission
Submitted (07-AUG-1992) G. Wic
Molecular Biology, University
                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 7095)

Zauner, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.

Identification of two distinct microtubule binding doma
recombinant rat MAP 1B

Ed., J. Cell Biol. 57 (1), 66-74 (1992)
                                                                                                                                                                                                               Direct Submission
Submitted (07-AUG-1991) G. Wiche, Inst of Biochemistry, of Vienna, Waehringerstrasse 17, 1090 Vienna, AUSTRIA revised by [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
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R.norvegicus mRNA for microtubule associated X60370 X60371 X60550
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Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidae; Cyprininae;
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Glasgow, E. and Schechter, N.
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                                                                                               AUSTRIA
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/dev_stage="adult"
                                                          1..7095
                                                                         Location/Qualifiers
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IVVRTVETRDGEIIKESTTERKDLP"
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/translation="MGLNDRFASYIEKVRFLEQQNKNLVAELNQLRGKEPSRLGDIYQ
EELRELRQVDGLNAGKARLEIERDNLASDLATLKQRLQEENALRQEAENNLNYFRQD
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ALKEIRAQFEAMATSNMQETEEWYRSKFADLTDAAGRNAEALRQAKQEANEYRRQIQG
ATCDLESLRGSNESLERQLREMEERFAIETAGYQDTVARLEDEIQMLKEEMARHLQEY
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0..1099
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Pred. No. 3.26e-01;
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Vienna, Dr. Bohrgasse 9, 1030
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DEFINITION
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Matches 3
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Local Similarity 76.1%;
hes 35; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-JUL-1994) R.P. Hellens, John Innes Institute, Colney Lane, Norwich NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Magnoliopsida; Rutanae; Sapindales; Fabaceae; Papilionoideae;
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Pisum sativum
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/gene="CHS-1A"
join(1040..1217,1328..2319)
/gene="CHS-1A"
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                                                                                                                                                                                                                                                   KNIEKALVEAFOPLNISDYNSIFWIAHPGGPAILDQVEAKLGLKQRKMQATRHVLSEY
GNMSSACVLFILDEMRRKSKEDGLATTGEGLEWGVLFGFGPGLTVETVLLHSMAT"
                                                                                                                                                                                                                                                                                     PKLGKEAATKAIKEWGQPKSKITHLIFCTTSGVDMPGADYQLTKLLGLRPYVKRYMMY
QQGCFAGGTVLRLAKDLAENNKGARVLVVCSEITAVTFRGPSDTHLDSLVGQALFGDG
AAAVIVGSDPLPDVEKPLFELVWTAQTIVPDSEGAIDGHLREAGLTFHLLKDVPSLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="linkage group 3" <1040..1217
                                                                                                                                                                                                                                                                                                                                          /product="naringenin-chalcone synthase"
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NSOHKTELKEKFORMCDKSMIKKRYMHLTEEILKENPSLCEYMAPSLDARODMVVVEV
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1856 c 1799 g 1
                                                                   /gene="CHS-1B"
join(4336..4513,4642..5633)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism-"Pisum sativum"
/strain-"JI 813"
/clone_lib-"labda GEM-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CHS-1A"
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Pred. No. 1.38e+00;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger Centre,
Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
Jes@sanger.ac.uk or rw@nematode.wustl.edu

2  (bases 1 to 18632)
Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Wilson,R., Surton,J., Conneell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
Staden,R., Sulston,J., Theory Miegy,J., Thomas,K., Vaudin,M.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Valkinson-Sproat,J. and Wohldman,P.
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note. IMPORTANT: This sequence is NOT necessarily the entire insert of clone C29F3. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green, ms in preparation), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEUZYF3 18632 bp DNA
Caenorhabditis elegans cosmid
Z81043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditc Rhabditidae; Peloderinae; Caenorhabditis.
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Similarity 81.6%;
31; Conservative
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4642..>5633
/gene="CHS-1B"
/number=2
a 1307 c 126
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NSEHKTELKEKFQRMCDKSMIKKTYMHLTEEILKENPSVCYMAPSLDARQDMVVYVV
PKLGKBAATRAIKENGQPKSKITHLIFCTTSGVDMPGADYQLTKLLGLRAPVKRYMMY
QQGCFAGGTVLRLAKDLAENNKGARVLVYCSEITAVTFRGPSDTHLDSLVGQALFGDG
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/gene="CHS-1B"
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KNIEKALVEAFQPLGISDINSLFWIAHPGGPAILDQVEAKLSLKQRKMQATRHVLSEY
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Pred. No. 1.38e+00;
Wismatches 7;
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RKGFISSDSYGNSFOEAFHINAPVKNDTIFKNNIATADLSGSTTLIVYCYRYILLTR
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QFLHIGAIRSCAAPPCATTDPYVWQNGVSNDNNFANDYIQLYDGSGQCLSMDLAKNGE
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HGKETTYSPVKYWLHRDPEQEAEFVEFLLENGESFTLTEKHLVFATDCQQNVKNLDDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MHWRLTVLFFASAQLSEGCLPMVPPEEPVTPVPVCPAGWFQFQRATGLWCYIFATPGAGGWTTPQAACQANYGANLNGFESAAERTQFIQDMLASNLAPYTFVHIGAWRQCAPCTVNDPFVWLNGVSNDNTFANDYDSLYDLTGDCLSMDLGNNGQYNDIT
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6642..6740))
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RESTDRNIATVSAGEIVIGGEVYQNESQYADAYISNIEXAGEVYYEVNIRRFAC
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LEEIIAQQGFIVENETTVAPFAGPFQAQGFQPRFGAPQGFQPAFQQPPPQQFFPQNFQ
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                                                                                                                                                                                17376..18179))
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                                                                                                                                                                                                                                                   complement(join(15422..15713,16068..16591,16640..17140,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=
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13344..13893,13948..14262,14952..15141)
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REFERENCE
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                                    KEYWORDS
                                                                           ACCESSION
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                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-NOV-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
Order of segments is not known; 800 n's separate segments.
Order of segments is not known; 800 n's separate segments.
Cosmid=T09D4; Contig ID=01673; Length=1019; Status=Unfinished
Cosmid=T09D4; Contig ID=01596; Length=1655; Status=Unfinished
Cosmid=T09D4; Contig ID=01600; Length=1271; Status=Unfinished.
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HTGS; HTG
                          g1780984
HTG; HTGS_PHASE1.
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                                                                                                              Human DNA sequence
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Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
Rhabditidae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                     1.6%;
Similarity 90.0%;
27; Conservation
                  human.
                                                                                           799F10; HTGS phase 1.
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larity 90.0%;
Conservative
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IAVNNKKTLLGLPEVTLGIMPODGGTORLPKLTTVQNVLLDLTLGKRIKANKIGI
VDRVIQPLGDGICTSTETTHKYLEIIAVOSARELANGKLVINIDKGFVHNATQAVMTS
KFVLDNVILKMAKNKLIKLTNGNYPAPLKILDVVRTAYLDPKNGYEAEAKAFGELSOT
FOSKALFGLFEGSTNAKKNKYGKGLPVNEIAVVGAGFMCAGIANVTINKGIRTVLLDA
NQAGVERGQNHYATHLMRQLKROKISKLEREKIYNHLVPTIDYSAMKNADVVIEAVFE
DLPLKHKVIRQIENVVGPNIIASNTSALPIKDIAAASSRSDKYGMMYFSVVLEAVFE
DLPLKHKVIRQIENVGPNILASNTSALPIKDIAAASSRSDKYGMMYFSVVLEKMQL
LEIITHDGTSKETLATAAQLGLKQGKLVVVVKDCPGFFVVRCLSPMMSEIVRLLQEGV
EPSELDKLTTKFGFPVGAATLADEAGLDVAEHVARYLGTALGPRVHGGSVDLLKSELVR
AGHKGEKTSKGIFYYGDGAKGSKKVNQEAAKLFEKYKLTPIKSYSSPEDRQLRLVSRF
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8322 c 831
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Pred. No. 1.38e+00;
0; Mismatches 3
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Homo sapiens

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RESULT 14
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formaldehyde dehydrogenase; ABC transporter; DNA ligase; DNA polymerase III alpha subunit; GumB protein; LysR transcriptional regulator; Mg-protoporhyrin IX; N-acetylornithine aminotransferase; NADH dehydrogenase subunit 4; NADH dehydrogenase subunit 5; acetate kinase; aspartoacylase(ASP); cation-transporting Affase; cell division protein FtsH; chemotaxis protein Chah; cytochrome oxidase d subunit I; cytochrome oxidase d subunit II; dienelactone hydrolase; dihydroflavonol 4-reductase; dihydropteroate pyrophosphorylase; esterase; ferrous iron transport protein B; fibrillin; formaldehyde dehydrogenase (glutathione); high light-inducible protein; leader peptidase I; lysostaphin; malonyl coenzyme A-acyl carrier protein transacylase; methyl-accepting chemotaxis protein (MCP); oligopeptide transport ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTTGTTTTGATGTTTCCATAACTTCAGCAGCTGGAAAG 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D90904 150894 bp DNA BCT 20-NOV-1996
Synechocystis sp. PCC6803 complete genome, 6/27, 630555-781448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * This sequence is unfinished. When sequencing is complete, 
* the sequence data presented in this record will be replac 
*by a single finished sequence with the same accession number.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of segments is not known; sequence: BK799F10 Contic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent the correct sequence. Work on the sequence is in progress
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Vertebrata;
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Similarity 80.0%;
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BK799F1
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/clone="799F10"
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28425 c 26764
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No. 1.38e+00;
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38510 bp Unfinished
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2254 bp Unfinished
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protein OppF; oxygen independent coprophorphyrinogen III oxidase; penicillin-binding protein 1B; phenoxybenzoate dioxygenase; phycocyanin a subunit; phycocyanin associated linker protein; phycocyanin b subunit; phycocyanin associated linker protein; phycocyanin b subunit; potassium channel; protein conferring resistance to acetazolamide, Zam; regulatory component of sensory transduction system; regulatory components of sensory transduction system; rigulatory components of sensory transduction system; ribonuclease II; sensory transduction histidine kinase; serine esterase; serine/threonine protein kinase; seryl-tana synthetase; sprulation protein SpoIID; sulfolipid biosynthesis sprotein sqdb; tana-arg; tana-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tabata,S.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF_ID:slr1019"
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RLKALLAEAGIDV"
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AUTHORS
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LOCUS
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Note: remainder of annotations omitted
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Best Local Similarity 81.6%;
Matches 31; Conservative
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Direct Submission

Submitted (06-MAY-1988) Cozzone A.J., University of Lyon,

Laboratory of Molecular Biology, 43 Boulevard du onze Novembre,
69622 Villeurbanne, France
2 (bases 1 to 1344)

Rieul,C., Bleicher,F., Duclos,B., Cortay,J.C. and Cozzone,A.J.

Nucleotide sequence of the aceA gene coding for isocitrate lyas
                                                    Nucleotide sequence of the aceA gene co
Escherichia coli
Nucleic Acids Res. 16 (12), 5689 (1988)
88262573
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Cozzone, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
Eubacteria; Proteobacteria;
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Location/Qualifiers
1..1344
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Pred. No. 1.38e+00;
0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           For isocitrate lyase (EC 4.1.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision;
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                                                                                                                                     isocitrate lyase in
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Search completed: Thu Aug 21 10:01:07 1997 Job time : 2597 secs.
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                                                                                                             983 cttataactgctcgccgtcgttcaactggcagaaaaa 1019
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1488 CTTATTACTGCTTGCAGTAATTCAACTGGAAAAAAAA 1524
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